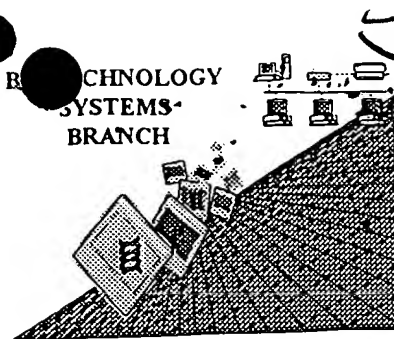


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/857557

Source: PCT 09

Date Processed by STIC: 10/29/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/957557

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001

TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt

Output Set: N:\CRF3\10292001\I857557.raw

3 <110> APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
 5 <120> TITLE OF INVENTION: PLANT 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE
 7 <130> FILE REFERENCE: BB1297
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/857,557
 C--> 10 <141> CURRENT FILING DATE: 2001-09-22
 12 <150> PRIOR APPLICATION NUMBER: 60/110,865
 W--> 13 <151> PRIOR FILING DATE: 1998-DECEMBER-04
 15 <160> NUMBER OF SEQ ID NOS: 22
 17 <170> SOFTWARE: Microsoft Office 97
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 565
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Zea mays
 24 <220> FEATURE:
 25 <221> NAME/KEY: unsure
 26 <222> LOCATION: (5)..(9)
 28 <220> FEATURE:
 29 <221> NAME/KEY: unsure
 30 <222> LOCATION: (450)
 32 <220> FEATURE:
 33 <221> NAME/KEY: unsure
 34 <222> LOCATION: (549)
 36 <400> SEQUENCE: 1
 W--> 37 aatgnnnnna tcaggctgtt acataggggg gcttgcatgt tacacaccca acctggccta 60
 38 gcctacccta ctacactcgt gcgattcgg cagcagcagc gacggtcgcc accaccgctc 120
 39 cccctccctct cccctcctc gccagcggc aattaccaca gcctccccag caagccggga 180
 40 tggctgcact caaggcatcg ttccgggggtg agctcagcgc cgttccttc ctcgactcca 240
 41 gcaggggacc tctcgtccag cacaagtggt attttacgtt tcaaaggaag ggcaaacgag 300
 42 ctatttcact gagaaggaca tgcgtttcta tgcaacaggc tccaccacca gcatggcctg 360
 43 ggcgagctgt tgcctgagcct ggccggagtc atgggatggc ccaaagccta tctcgattgt 420
 W--> 44 tgggttcaact ggttccatag gaacacagan attggacatt gttgcggaga atcctgataa 480
 45 gttcagagtt gttgctcttg ctgctggatc caatgtcagc cttctagctg atcaggtcaa 540
 W--> 46 aacattcaaa cctaagttgg ttccgg 565
 48 <210> SEQ ID NO: 2
 49 <211> LENGTH: 63
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Zea mays
 53 <220> FEATURE:
 54 <221> NAME/KEY: UNSURE
 55 <222> LOCATION: (25)
 57 <220> FEATURE:
 58 <221> NAME/KEY: UNSURE
 59 <222> LOCATION: (58)
 61 <400> SEQUENCE: 2
 62 Ala Trp Pro Glu Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile Val Gly
 63 1 5 10 15
 W--> 65 Ser Thr Gly Ser Ile Gly Thr Gln Xaa Leu Asp Ile Val Ala Glu Asn

1998-12-04
 Edit date format

Does Not Comply
 Corrected Diskette Needed

② Enumerate Unknown
 in feature
 221, 222 and 223
 for protein and nucleotide
 sequences.

Field 223 is
 required

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

Field 223 is required

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001

TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt

Output Set: N:\CRF3\10292001\I857557.raw

```

66          20          25          30
68 Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
69          35          40          45
W--> 71 Leu Leu Ala Asp Gln Val Lys Thr Phe Xaa Pro Lys Leu Val Arg
72          50          55          60
74 <210> SEQ ID NO: 3
75 <211> LENGTH: 868
76 <212> TYPE: DNA
77 <213> ORGANISM: Zea mays
79 <220> FEATURE:
80 <221> NAME/KEY: unsure
81 <222> LOCATION: (343)
83 <220> FEATURE:
84 <221> NAME/KEY: unsure
85 <222> LOCATION: (356)
87 <220> FEATURE:
88 <221> NAME/KEY: unsure
89 <222> LOCATION: (367)
91 <220> FEATURE:
92 <221> NAME/KEY: unsure
93 <222> LOCATION: (789)
95 <220> FEATURE:
96 <221> NAME/KEY: unsure
97 <222> LOCATION: (862)
99 <400> SEQUENCE: 3
100 gatgaattga aagaagcctt ggctgattgc gaagagaagc cagaaattat tcctggggag 60
101 caaggtgtca tagaagttgc tcgccatcca gatgcagtta cagttgtcac agggatagta 120
102 ggttgtgcag ggctgaagcc tacagttgct gcaattgaag ctggtaaaga catagcattg 180
103 gcaaacaaag agacacttat tgcaggtggt ccttttgtgc ttcccttgc acacaaacac 240
104 aaagtgaaaa ttcttcacgc tgattctgag cactctgcaa tatttcagt tatacaaggc 300
W--> 105 ttgtccgaag gtgcacttcg tcgcattatt ctaactgcat cagtgggtgc tttcaggac 360
W--> 106 tggccfnttg acaggctgaa agatgtaaaa gttgctgacg ctttaaagca tccaaactgg 420
107 aatatgggaa ggaagatcac agtagattct gctactttat tcaacaaggg tttagaagtt 480
108 attgaagcac attatttatt tgggtgctgaa tatgatgaca ttgagattgt gattcaccca 540
109 cagtctatca tacactctat ggttgaaacc caggattcat ctgtcctagc tcagttggga 600
110 tggccagata tgcggttacc aatcttatac accttatcat ggccagatag gagtcctgag 660
111 cgctgctaata gagaaggccg tggagttggt cattgacgag aagattagct acctggacat 720
112 attcaagggtg gtggagctta catgtaacgc gcatcggaac agctggtaac aaccgtcact 780
W--> 113 ggagggaatg tcattacatc gtggcaagaa tatgcagcat cacaacatct ctggctgagc 840
W--> 114 tgtcctgcat atagtctcac anacttgt 868
116 <210> SEQ ID NO: 4
117 <211> LENGTH: 217
118 <212> TYPE: PRT
119 <213> ORGANISM: Zea mays
121 <220> FEATURE:
122 <221> NAME/KEY: UNSURE
123 <222> LOCATION: (115)
125 <220> FEATURE:
126 <221> NAME/KEY: UNSURE

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001

TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt

Output Set: N:\CRF3\10292001\I857557.raw

```

127 <222> LOCATION: (119)
129 <220> FEATURE:
130 <221> NAME/KEY: UNSURE
131 <222> LOCATION: (123)
133 <400> SEQUENCE: 4
134 Asp Glu Leu Lys Glu Ala Leu Ala Asp Cys Glu Glu Lys Pro Glu Ile
135   1          5          10          15
137 Ile Pro Gly Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Asp Ala
138          20          25          30
140 Val Thr Val Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr
141          35          40          45
143 Val Ala Ala Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu
144          50          55          60
146 Thr Leu Ile Ala Gly Gly Pro Phe Val Leu Pro Leu Ala His Lys His
147          65          70          75          80
149 Lys Val Lys Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln
150          85          90          95
152 Cys Ile Gln Gly Leu Ser Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr
153          100          105          110
W--> 155 Ala Ser Xaa Gly Ala Phe Xaa Asp Trp Pro (Xaa) Asp Arg Leu Lys Asp
156          115          120          125
158 Val Lys Val Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Arg
159          130          135          140
161 Lys Ile Thr Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val
162          145          150          155          160
164 Ile Glu Ala His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile
165          165          170          175
167 Val Ile His Pro Gln Ser Ile Ile His Ser Met Val Glu Thr Gln Asp
168          180          185          190
170 Ser Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile
171          195          200          205
173 Leu Tyr Thr Leu Ser Trp Pro Asp Arg
174          210          215
176 <210> SEQ ID NO: 5
177 <211> LENGTH: 1901
178 <212> TYPE: DNA
179 <213> ORGANISM: Oryza sativa
181 <400> SEQUENCE: 5
182 acactatgac catgattacg ccaagcgcgc aattaaccct cactaaaggg aacaaaagct 60
183 ggagctccac cgcggtggcg gccgctctag aactagtgga tccccgggc tgcaggaatt 120
184 cggcacgagg tttaaaccag acgtcgagtc gagcattaac tcagtcaggg tggccatggc 180
185 gctcaaggtc gtctctttcc cgggggactt ggccgcggtc tcattcctcg actccaacag 240
186 aggaggagct ttcaaccagc tcaaagtgga cctcccgttt caaacgaggg acagaagagc 300
187 agtttccctg agaaggactt gctgttcaat gcaacaggct ccaccaccag catggcctgg 360
188 tcgagccgtt gttgaacctg ggaggaggtc atgggatggc cccaagccta tctcaattgt 420
189 tggtcaacc ggttctattg gcacacagac attggacata gttgcggaga atccagataa 480
190 attccgggtt gttgctcttg ctgctggctc caatgtgact cttctagctg atcaggtgaa 540
191 aacattcaaa ccaaagcttg ttgctgtaag aaatgagtca ttagttgatg agctaaagga 600
192 agccttagct gattgtgatt ggaagccaga aattattcct ggtgagcaag gtgtcataga 660

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001

TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt

Output Set: N:\CRF3\10292001\I857557.raw

```

193 ggttgctcgc caccagatg cagttacagt tgttactggg atagtagggg gtgcaggact 720
194 gaagcctaca gttgctgcaa ttgaagctgg gaaagatata gcattggcga acaaagagac 780
195 acttattgca ggtggtcctt ttgtgcttcc ccttgacaaa aagcacaaag tgaaaatact 840
196 tctgtctgat tctgagcaact ctgctatatt tcagtgtata caaggcttgc ccgaaggagc 900
197 acttcgccgc attattttga ctgcatcagg tgggtgctttc agggactggc cagttgacaa 960
198 gttgaaagaa gtaaaagttg ctgatgcttt aaagcacccg aactggaata tggggaagaa 1020
199 gattactgta gattctgcta cattattcaa caagggttta gaagttattg aagcacatta 1080
200 tttatttggg gctgaatacg atgacattga aattgtgatc caccacaat ctatcataca 1140
201 ctctatgatt gaaacccagg attcatctgt gttggctcaa ctgggatggc cagatatgcy 1200
202 gataccaacc ttatacacca tgtcttggcc agacagaatc tattgctcag aggtcacctg 1260
203 gcccgacta gatctttgca agctgggttc actgacattc aaagctcctg acaatgtgaa 1320
204 ataccgctcg atggatctcg cctatgcagc tggaagagct gggggcacca tgacaggagt 1380
205 tctgagtget gctaatagaga aggtgtgga gttgttcac gatgaaaaga tcgggtacct 1440
206 ggacatcttc aaggtggtgg agctgacatg cgacgctcat cggaatgagc tagtaacaag 1500
207 gccatcactg gaggagatca tacattatga tctgtgggcy agggagtatg ctgccagcct 1560
208 acagccatcc actggcctca gccctgtacc tgtctagtac ttgtagcaat acaaaattac 1620
209 agtagcattg tacactactg ccgtgccagc tccatgcata gtcagcagct ggccactctc 1680
210 tagctatctc tagatgcgag agaattttaa ggatgtaaat catgccttca catgaataaa 1740
211 tcgttcgtcc gtgcgttgtg tattcatgta aattttgacg gatggtcaag taaaaataac 1800
212 aatggcaaat taatttaggg aaaaaaaaaa aaaaaaaact cgaggggggg cccggtacct 1860
213 aattcgccct atagtgaagc gtattacgcy cgctcactgg c 1901

```

215 <210> SEQ ID NO: 6

216 <211> LENGTH: 473

217 <212> TYPE: PRT

218 <213> ORGANISM: Oryza sativa

220 <400> SEQUENCE: 6

```

221 Met Ala Leu Lys Val Val Ser Phe Pro Gly Asp Leu Ala Ala Val Ser
222 1 5 10 15
224 Phe Leu Asp Ser Asn Arg Gly Gly Ala Phe Asn Gln Leu Lys Val Asp
225 20 25 30
227 Leu Pro Phe Gln Thr Arg Asp Arg Ala Val Ser Leu Arg Arg Thr
228 35 40 45
230 Cys Cys Ser Met Gln Gln Ala Pro Pro Pro Ala Trp Pro Gly Arg Ala
231 50 55 60
233 Val Val Glu Pro Gly Arg Arg Ser Trp Asp Gly Pro Lys Pro Ile Ser
234 65 70 75 80
236 Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val
237 85 90 95
239 Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser
240 100 105 110
242 Asn Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu
243 115 120 125
245 Val Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu
246 130 135 140
248 Ala Asp Cys Asp Trp Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val
249 145 150 155 160
251 Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile
252 165 170 175
254 Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001

TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt

Output Set: N:\CRF3\10292001\I857557.raw

```

255          180          185          190
257 Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro
258          195          200          205
260 Phe Val Leu Pro Leu Ala Gln Lys His Lys Val Lys Ile Leu Pro Ala
261          210          215          220
263 Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu
264 225          230          235          240
266 Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg
267          245          250          255
269 Asp Trp Pro Val Asp Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu
270          260          265          270
272 Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala
273          275          280          285
275 Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe
276          290          295          300
278 Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile
279 305          310          315          320
281 Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu
282          325          330          335
284 Gly Trp Pro Asp Met Arg Ile Pro Thr Leu Tyr Thr Met Ser Trp Pro
285          340          345          350
287 Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys
288          355          360          365
290 Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro
291          370          375          380
293 Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr
294 385          390          395          400
296 Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp
297          405          410          415
299 Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys
300          420          425          430
302 Asp Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile
303          435          440          445
305 Ile His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala Ser Leu Gln Pro
306          450          455          460
308 Ser Thr Gly Leu Ser Pro Val Pro Val
309 465          470
311 <210> SEQ ID NO: 7
312 <211> LENGTH: 1592
313 <212> TYPE: DNA
314 <213> ORGANISM: Glycine max
316 <220> FEATURE:
317 <221> NAME/KEY: unsure
318 <222> LOCATION: (993)
320 <220> FEATURE:
321 <221> NAME/KEY: unsure
322 <222> LOCATION: (1402)
324 <400> SEQUENCE: 7
325 gctggttcaa ctgaggtgat ggctttgaat ttgccttctc ccgcccaagt gaagccctta 60

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001

TIME: 13:15:17

Input Set : A:\BB1297 PCT Seq List.txt

Output Set: N:\CRF3\10292001\I857557.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:37 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:65 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:71 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:105 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:113 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:114 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:155 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:341 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:348 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:427 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:451 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:521 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:531 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:532 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:533 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:553 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:583 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:650 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:651 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001

TIME: 13:15:17

Input Set : A:\BB1297 PCT Seq List.txt

Output Set: N:\CRF3\10292001\I857557.raw

L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:652 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:708 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:709 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:730 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:749 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15